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 Leu Asn Val Ile Thr Thr Asn His Ile Leu Ser Asn Cys  
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gag ctg gtt aag aag ttt tta gat cca aac aac tat tcc 440  
 Glu Leu Val Lys Lys Phe Leu Asp Pro Asn Asn Tyr Ser  
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gca aac tat act gag att gcc ttg caa cag gtt tcc atg 479  
 Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln Val Ser Met  
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ttc ttc cga tca gaa cca aag tgg gag gtg gtg gaa cct 518  
 Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu Pro  
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ttg aaa gac ata ggt tgg aga ata agg aag aaa tat ttc 557  
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ttg atg aag att aaa aat cag cca aag gaa cgg cta gtg 596  
 Leu Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val  
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tta agc tgg gct gac ctt ggc cca gac aag tat ttg tca 635  
 Leu Ser Trp Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser  
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gat aaa gat ttt cag tgt cta atc aaa ctt ctg cct tct 674  
 Asp Lys Asp Phe Gln Cys Leu Ile Lys Leu Leu Pro Ser  
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tgt ttg cac cct tac atc tat cgg gtt acc ttt gcc aca 713  
 Cys Leu His Pro Tyr Ile Tyr Arg Val Thr Phe Ala Thr  
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gct aat gaa tcc tca gcg ttg cta att agg atg ttt aac 752  
 Ala Asn Glu Ser Ser Ala Leu Leu Ile Arg Met Phe Asn  
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gaa aag gga aca ttg aag gat ctg atc tac aag gca aaa 791  
 Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys Ala Lys  
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cca aaa gac cca ttt cta aag aag tac tgc aac cct aag 830  
 Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys  
 245 250 255

aag att cag ggc ctg gaa ctc cag caa ata aaa aca tat 869  
 Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr  
 260 265

gga cgg caa ata tta gag gta ctg aag ttt ctt cat gac 908  
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 270 275 280

aag gga ttc cct tat ggg cat ctt cac gcc tcc aat gtg 947  
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atg ctc gat ggg gac act tgt cgg ctg ctg gac ctt gag 986  
 Met Leu Asp Gly Asp Thr Cys Arg Leu Leu Asp Leu Glu  
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aat tcc tta ttg ggc ctg cct tcc ttc tac cga tct tat 1025  
 Asn Ser Leu Leu Gly Leu Pro Ser Phe Tyr Arg Ser Tyr  
 310 315 320

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 Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu Glu Ser Val  
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tat gga cga ccg cca gac tcg gtg cct gtg gac tcc ttc 1142  
 Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe  
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cct cct gcc ccg tcc atg gct gtg gtg gcc gtg ttg gag 1181  
 Pro Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu  
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 Ser Thr Leu Ser Cys Glu Ala Cys Lys Asn Gly Met Pro  
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acc atc tcc cgg ctc tta cag atg cca tta ttc agc gat 1259  
 Thr Ile Ser Arg Leu Leu Gln Met Pro Leu Phe Ser Asp  
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gtt tta cta acc act tct gaa aaa cca cag ttt aag atc 1298  
 Val Leu Leu Thr Thr Ser Glu Lys Pro Gln Phe Lys Ile  
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cct aca aag tta aaa gag gca ttg aga att gcc aaa gaa 1337  
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cac cag cat cga aga ctg aca aga gct cag tcc cac cat 1415  
 His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His  
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gga tct gag gag gaa aga aaa aaa aga aag att tta gct 1454  
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 Arg Lys Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu  
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Ser Gly Ala Ser Ser Pro Leu Thr Ser Pro Ser Ser Pro  
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 Thr Pro Pro Ser Thr Ser Gly Ile Ser Ala Leu Pro Pro  
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 Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser Gln  
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 Thr Cys Asp His Ser Ala Pro Lys Ile Gly  
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Val Glu Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp  
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Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu Pro Leu  
65 70 75  
Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg Glu Phe Ile Ala  
80 85 90  
Glu Arg Gln Lys Gly Leu Gln Asn Tyr Leu Asn Val Ile Thr Thr  
95 100 105  
Asn His Ile Leu Ser Asn Cys Glu Leu Val Lys Lys Phe Leu Asp  
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Pro Asn Asn Tyr Ser Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln  
125 130 135  
Val Ser Met Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu  
140 145 150  
Pro Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe Leu  
155 160 165  
Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val Leu Ser Trp  
170 175 180  
Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser Asp Lys Asp Phe Gln  
185 190 195  
Cys Leu Ile Lys Leu Leu Pro Ser Cys Leu His Pro Tyr Ile Tyr  
200 205 210  
Arg Val Thr Phe Ala Thr Ala Asn Glu Ser Ser Ala Leu Leu Ile  
215 220 225

Arg	Met	Phe	Asn	Glu	Lys	Gly	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Lys	230	235	240
Ala	Lys	Pro	Lys	Asp	Pro	Phe	Leu	Lys	Lys	Tyr	Cys	Asn	Pro	Lys	245	250	255
Lys	Ile	Gln	Gly	Leu	Glu	Leu	Gln	Gln	Ile	Lys	Thr	Tyr	Gly	Arg	260	265	270
Gln	Ile	Leu	Glu	Val	Leu	Lys	Phe	Leu	His	Asp	Lys	Gly	Phe	Pro	275	280	285
Tyr	Gly	His	Leu	His	Ala	Ser	Asn	Val	Met	Leu	Asp	Gly	Asp	Thr	290	295	300
Cys	Arg	Leu	Leu	Asp	Leu	Glu	Asn	Ser	Leu	Leu	Gly	Leu	Pro	Ser	305	310	315
Phe	Tyr	Arg	Ser	Tyr	Phe	Ser	Gln	Phe	Arg	Lys	Ile	Asn	Thr	Leu	320	325	330
Glu	Ser	Val	Asp	Val	His	Cys	Phe	Gly	His	Leu	Leu	Tyr	Glu	Met	335	340	345
Thr	Tyr	Gly	Arg	Pro	Pro	Asp	Ser	Val	Pro	Val	Asp	Ser	Phe	Pro	350	355	360
Pro	Ala	Pro	Ser	Met	Ala	Val	Val	Ala	Val	Leu	Glu	Ser	Thr	Leu	365	370	375
Ser	Cys	Glu	Ala	Cys	Lys	Asn	Gly	Met	Pro	Thr	Ile	Ser	Arg	Leu	380	385	390
Leu	Gln	Met	Pro	Leu	Phe	Ser	Asp	Val	Leu	Leu	Thr	Thr	Ser	Glu	395	400	405
Lys	Pro	Gln	Phe	Lys	Ile	Pro	Thr	Lys	Leu	Lys	Glu	Ala	Leu	Arg	410	415	420
Ile	Ala	Lys	Glu	Cys	Ile	Glu	Lys	Arg	Leu	Ile	Glu	Glu	Gln	Lys	425	430	435
Gln	Ile	His	Gln	His	Arg	Arg	Leu	Thr	Arg	Ala	Gln	Ser	His	His	440	445	450
Gly	Ser	Glu	Glu	Glu	Arg	Lys	Lys	Arg	Lys	Ile	Leu	Ala	Arg	Lys	455	460	465
Lys	Ser	Lys	Arg	Ser	Ala	Leu	Glu	Asn	Ser	Glu	Glu	His	Ser	Ala	470	475	480
Arg	Tyr	Ser	Asn	Ser	Asn	Asn	Ser	Gly	Ser	Gly	Ala	Ser	Ser	Pro	485	490	495
Leu	Thr	Ser	Pro	Ser	Ser	Pro	Thr	Pro	Pro	Ser	Thr	Ser	Gly	Ile	500	505	510
Ser	Ala	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ala	515	520	525
Pro	Leu	Pro	Pro	Ala	Ser	Thr	Glu	Val	Pro	Ala	Gln	Leu	Ser	Ser			

530	535	540
Gln Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser Ile		
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Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys Thr Cys Asp		
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His Ser Ala Pro Lys Ile Gly		
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 gtgaacatag atacagctct ttcccccttc cccccctttt aaatgtaaca 150  
 aatacttttt atgttccccct tcccccttcc ccctttttccc ctttccccctt 200  
 ttggaaacgt gtcaggaacc aaatagttta agatgagcag ttgagggggac 250  
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 cgtgctgccg gccagggttac ttaagcacc ttttaacaag gaaaccttgt 350  
 gggagatcca gctggccgac tcgagttcag aaacaggacc acagagggtta 400  
 cactctggga tcctggccat gaggttggat gcctcacctt actgaaagga 450  
 gacactggac ctaa atg gcg cag cat gat ttt gtt cct gct 491  
 Met Ala Gln His Asp Phe Val Pro Ala  
 1 5  
 tgg cta aat ttc tca aca cca cag tca gct aag tca cct 530  
 Trp Leu Asn Phe Ser Thr Pro Gln Ser Ala Lys Ser Pro  
 10 15 20  
 act gcc acc ttc gaa aaa cac gga gag cac cta ccc aga 569  
 Thr Ala Thr Phe Glu Lys His Gly Glu His Leu Pro Arg  
 25 30 35  
 gga gaa ggt aga ttt gga gta agc cgc cgt cga cat aat 608  
 Gly Glu Gly Arg Phe Gly Val Ser Arg Arg Arg His Asn  
 40 45  
 tcc tct gat ggt ttt ttt aac aat ggt ccc cta cga act 647  
 Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg Thr  
 50 55 60  
 gca gga gat tct tgg cac cag ccc tcc tgt tcc gcc atg 686  
 Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met  
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 att ctg tgg act ctg gtg tct cta agg gag cat atg ctg 725  
 Ile Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu

75		80		85	
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Glu Ser Gln Gly Thr His Leu Val Gly Ile Ala Leu Pro					
90		95		100	
cga ggt cat gat ggc atg agc caa cgt agt gta ggt ggc	803				
Arg Gly His Asp Gly Met Ser Gln Arg Ser Val Gly Gly					
105		110			
aca ggg aac cat cgc cat tgg aat ggc agc ttc cac tcc	842				
Thr Gly Asn His Arg His Trp Asn Gly Ser Phe His Ser					
115		120		125	
cgg aaa ggg tgt gct ttt cag gaa aag cca cct atg gag	881				
Arg Lys Gly Cys Ala Phe Gln Glu Lys Pro Pro Met Glu					
130		135			
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Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu Lys Leu					
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cag ttt gaa gag gag gac ttt cct tcc ttg aat cca gaa	959				
Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu					
155		160		165	
gct ggc aaa cag cat cag cca tgc aga cct att ggg aca	998				
Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr					
170		175			
cct tct gga gta tgg gaa aac ccg cct agt gcc aag caa	1037				
Pro Ser Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln					
180		185		190	
ccc tcc aag atg cta gtt atc aaa aaa gtt tcc aaa gag	1076				
Pro Ser Lys Met Leu Val Ile Lys Lys Val Ser Lys Glu					
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Asp Pro Ala Ala Ala Phe Ser Ala Ala Phe Thr Ser Pro					
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gga tct cac cat gca aat ggg aac aaa ttg tca tcc gtg	1154				
Gly Ser His His Ala Asn Gly Asn Lys Leu Ser Ser Val					
220		225		230	
gtt cca agt gtc tat aag aac ctg gtt cct aag cct gta	1193				
Val Pro Ser Val Tyr Lys Asn Leu Val Pro Lys Pro Val					
235		240			
cca cct cct tcc aag cct aat gca tgg aaa gct aac agg	1232				
Pro Pro Pro Ser Lys Pro Asn Ala Trp Lys Ala Asn Arg					
245		250		255	
atg gag cac aag tca gga tcc ctt tcc tct agc cgg gag	1271				
Met Glu His Lys Ser Gly Ser Leu Ser Ser Ser Arg Glu					
260		265			
tct gct ttt acc agt cca atc tcc gtt acc aaa cca gtg	1310				
Ser Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro Val					
270		275		280	

gta ctg gct agt ggt gca gct ctg agt tct ccc aaa gag 1349  
 Val Leu Ala Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu  
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agt ccc tcc agc acc acc cct cca att gag atc agc tcc 1388  
 Ser Pro Ser Ser Thr Thr Pro Pro Ile Glu Ile Ser Ser  
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tct cgt ctg acc aag ttg acc cgc cga acc acc gac agg 1427  
 Ser Arg Leu Thr Lys Leu Thr Arg Arg Thr Thr Asp Arg  
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aag agt gag ttc ctg aaa act ctg aag gat gac cgg aat 1466  
 Lys Ser Glu Phe Leu Lys Thr Leu Lys Asp Asp Arg Asn  
 325 330

gga gac ttc tca gag aat aga gac tgt gac aag ctg gaa 1505  
 Gly Asp Phe Ser Glu Asn Arg Asp Cys Asp Lys Leu Glu  
 335 340 345

gat ttg gag gac aac agc aca cct gaa cca aag gaa aat 1544  
 Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn  
 350 355 360

ggg gag gaa ggc tgt cat caa aat ggt ctt gcc ctc cct 1583  
 Gly Glu Glu Gly Cys His Gln Asn Gly Leu Ala Leu Pro  
 365 370

gta gtg gaa gaa ggg gag gtt ctc tca cac tct cta gaa 1622  
 Val Val Glu Glu Gly Glu Val Leu Ser His Ser Leu Glu  
 375 380 385

gca gag cac agg tta ttg aaa gct atg ggt tgg cag gaa 1661  
 Ala Glu His Arg Leu Leu Lys Ala Met Gly Trp Gln Glu  
 390 395

tat cct gaa aat gat gag aat tgc ctt ccc ctc aca gag 1700  
 Tyr Pro Glu Asn Asp Glu Asn Cys Leu Pro Leu Thr Glu  
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gat gag ctc aaa gag ttc cac atg aag aca gag cag ctg 1739  
 Asp Glu Leu Lys Glu Phe His Met Lys Thr Glu Gln Leu  
 415 420 425

aga aga aat ggc ttt gga aag aat ggc ttc ttg cag agc 1778  
 Arg Arg Asn Gly Phe Gly Lys Asn Gly Phe Leu Gln Ser  
 430 435

cgc agt tcc agt ctg ttc tcc cct tgg aga agc act tgc 1817  
 Arg Ser Ser Ser Leu Phe Ser Pro Trp Arg Ser Thr Cys  
 440 445 450

aaa gca gag ttt gag gac tca gac acc gaa acc agt agc 1856  
 Lys Ala Glu Phe Glu Asp Ser Asp Thr Glu Thr Ser Ser  
 455 460

agt gaa aca tca gat gac gat gcc tgg aag t agg 1890  
 Ser Glu Thr Ser Asp Asp Asp Ala Trp Lys  
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 ttcattcaca agggaaataa tcatatccca aagagagaaa aaaaaaaaaa 2040  
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 35 40 45  
 Arg His Asn Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg  
 50 55 60  
 Thr Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met Ile  
 65 70 75  
 Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu Glu Ser Gln  
 80 85 90  
 Gly Thr His Leu Val Gly Ile Ala Leu Pro Arg Gly His Asp Gly  
 95 100 105  
 Met Ser Gln Arg Ser Val Gly Gly Thr Gly Asn His Arg His Trp  
 110 115 120  
 Asn Gly Ser Phe His Ser Arg Lys Gly Cys Ala Phe Gln Glu Lys  
 125 130 135  
 Pro Pro Met Glu Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu  
 140 145 150  
 Lys Leu Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu  
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 Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr Pro Ser  
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 Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln Pro Ser Lys Met  
 185 190 195  
 Leu Val Ile Lys Lys Val Ser Lys Glu Asp Pro Ala Ala Ala Phe  
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 Ser Ala Ala Phe Thr Ser Pro Gly Ser His His Ala Asn Gly Asn  
 215 220 225

Lys	Leu	Ser	Ser	Val	Val	Pro	Ser	Val	Tyr	Lys	Asn	Leu	Val	Pro	230	235	240
Lys	Pro	Val	Pro	Pro	Pro	Ser	Lys	Pro	Asn	Ala	Trp	Lys	Ala	Asn	245	250	255
Arg	Met	Glu	His	Lys	Ser	Gly	Ser	Leu	Ser	Ser	Ser	Arg	Glu	Ser	260	265	270
Ala	Phe	Thr	Ser	Pro	Ile	Ser	Val	Thr	Lys	Pro	Val	Val	Leu	Ala	275	280	285
Ser	Gly	Ala	Ala	Leu	Ser	Ser	Pro	Lys	Glu	Ser	Pro	Ser	Ser	Thr	290	295	300
Thr	Pro	Pro	Ile	Glu	Ile	Ser	Ser	Ser	Arg	Leu	Thr	Lys	Leu	Thr	305	310	315
Arg	Arg	Thr	Thr	Asp	Arg	Lys	Ser	Glu	Phe	Leu	Lys	Thr	Leu	Lys	320	325	330
Asp	Asp	Arg	Asn	Gly	Asp	Phe	Ser	Glu	Asn	Arg	Asp	Cys	Asp	Lys	335	340	345
Leu	Glu	Asp	Leu	Glu	Asp	Asn	Ser	Thr	Pro	Glu	Pro	Lys	Glu	Asn	350	355	360
Gly	Glu	Glu	Gly	Cys	His	Gln	Asn	Gly	Leu	Ala	Leu	Pro	Val	Val	365	370	375
Glu	Glu	Gly	Glu	Val	Leu	Ser	His	Ser	Leu	Glu	Ala	Glu	His	Arg	380	385	390
Leu	Leu	Lys	Ala	Met	Gly	Trp	Gln	Glu	Tyr	Pro	Glu	Asn	Asp	Glu	395	400	405
Asn	Cys	Leu	Pro	Leu	Thr	Glu	Asp	Glu	Leu	Lys	Glu	Phe	His	Met	410	415	420
Lys	Thr	Glu	Gln	Leu	Arg	Arg	Asn	Gly	Phe	Gly	Lys	Asn	Gly	Phe	425	430	435
Leu	Gln	Ser	Arg	Ser	Ser	Ser	Leu	Phe	Ser	Pro	Trp	Arg	Ser	Thr	440	445	450
Cys	Lys	Ala	Glu	Phe	Glu	Asp	Ser	Asp	Thr	Glu	Thr	Ser	Ser	Ser	455	460	465
Glu	Thr	Ser	Asp	Asp	Asp	Ala	Trp	Lys							470		

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<211> 294

<212> DNA

<213> Homo sapiens

<220>

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 cccacacgga atatattatt cgagtgcaaa gaggaatttc tctggaaaac 150  
 agctggcaga tngtnagaag atacagtgcac tttnatntgc ttaacaacag 200  
 cttncanatt ncaggncatna gnntncctct tcctccnaan aaantgattn 250  
 ggnaacatgg ancgtnant tcatngctng anaggcaggn aggt 294

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 <213> Homo sapiens

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<210> 9  
 <211> 793  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 379, 433, 459, 492, 517, 541, 549, 561, 575, 579, 582, 710, 742,  
 774, 784  
 <223> unknown base

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 gacctattgg gacaccttct ggagtatggg aaaacccgcc tagtgccaag 150  
 caaccctcca agatgctagt tatcaaaaaa gtttccaaag aggatcctgc 200  
 tgctgcyttc tctgctgcat tcacctcacc aggatctcac catgcaaata 250

ggaacaaatt gtcatccgtg gttccaagtg tctataagaa cctgggttcc 300  
 aagcctgtac cacctccttc caagccta at gcatggaaag ctaacaggat 350  
 ggagcacaag tcaggatccc tttcctctna gccgggagtc tgcttttacc 400  
 agtccaatct ctgttacc aa accagtggta ctnggctagt ggtgcagctc 450  
 tgagttctnc ccaaagagag tccctccagc accaccctc cnaattgaga 500  
 tcagctcctc tcgtctngac caagtttgac ccgccgaacc naccgacang 550  
 gaagragtga ngttcctgaa aactnctgna anggatgacc gggaatggga 600  
 agacttityc agaagaatag agactgtgac aagctggaag atttgaggga 650  
 caacagcaca ctgaaccaa ggaaaatggg ggaggaaggc tgttcatcaa 700  
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<210> 11  
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 <212> DNA  
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<400> 12  
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 <222> 103  
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1						5						
cag gga gtg gtn cta aca gcc tac cac ccc agc ggc aag	130											
Gln Gly Val Xaa Leu Thr Ala Tyr His Pro Ser Gly Lys												
10 15 20												
gac cag acc gtc ggg aac agc cat gca aag gca ggg gag	169											
Asp Gln Thr Val Gly Asn Ser His Ala Lys Ala Gly Glu												
25 30												
gaa gcc acc tcg agt cgc aga tat ggc cag tac act atg	208											
Glu Ala Thr Ser Ser Arg Tyr Gly Gln Tyr Thr Met												
35 40 45												
aac cag gaa agc acc acc atc aaa gtt atg gag aag cct	247											
Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro												
50 55												
cca ttt gat cga tca att tcc cag gat tct ttg gat gaa	286											
Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu												
60 65 70												
cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc	325											
Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile												
75 80 85												
aag aaa tct agt gaa aac agc caa gaa gat caa gag gtg	364											
Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val												
90 95												
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Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu												
100 105 110												
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Glu Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly												
115 120												
gag tct gct gga gat cca cag gaa agc att gtg ttt tta	481											
Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile Val Phe Leu												
125 130 135												
tca aca ttg acg cgg acc cag gca gca gca gtt cag aag	520											
Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys												
140 145 150												
cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac	559											
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn												
155 160												
aaa cag tac cag att cct gac gtc aga gac ata ttt gct	598											
Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala												
165 170 175												
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Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr												
180 185												
gaa tcg cag tca ctt aga aca aat gaa aac aaa tac caa	676											
Glu Ser Gln Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln												

190		195		200	
gga aga gat gac gag gca tct aac ctt gtt ggt gaa gag	715				
Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu Glu					
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aag ctg atc cca cct gag gag acg cct gcc cct gaa aca	754				
Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr					
220		225			
gac atc aac ctg gag gta tca ttt gcc gag caa gca ctc	793				
Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu					
230		235		240	
aat cag aaa gag aga tcc aag gag aaa atc cag aag agc	832				
Asn Gln Lys Glu Arg Ser Lys Glu Lys Ile Gln Lys Ser					
245		250			
aaa ggc gat gat gcc aca tta cct agt ttc aga ttg cca	871				
Lys Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro					
255		260		265	
aaa gac aaa acg ggt acc aca agg att ggt gac ctc gca	910				
Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp Leu Ala					
270		275		280	
ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att	949				
Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile					
285		290			
gag ctg act gcc ctc tat gat gta ttg ggt att gag ctg	988				
Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu					
295		300		305	
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Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys Asp Ser					
310		315			
ggt ctt ttt tgc gtt cca ttg aca gcg cta tta gaa caa	1066				
Gly Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln					
320		325		330	
gat cag agg aaa gta cca gga atg cga ata ccc ttg atc	1105				
Asp Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile					
335		340		345	
ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg	1144				
Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu					
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gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att	1183				
Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile					
360		365		370	
aga atc aag aat ctt tgc caa gaa cta gaa gca aag ttt	1222				
Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe					
375		380			
tat gaa ggg act ttt aat tgg gaa agt gtc aaa cag cat	1261				
Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His					
385		390		395	

gat gcc gcc agc ctg ctg aag ctc ttc att cgg gag ttg 1300  
Asp Ala Ala Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu  
400 405 410

ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc ttt 1339  
Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala Phe  
415 420

cag gct gtc cag aat ctt cca acc aag aag cag caa cta 1378  
Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu  
425 430 435

cag gct ttg aac ctt ctt gtc atc ctc cta cct gat gca 1417  
Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala  
440 445

aac agg gac aca ctg aag gcc ctt ctt gaa ttt ctc caa 1456  
Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln  
450 455 460

aga gta ata gat aat aaa gaa aaa aat aaa atg aca gtc 1495  
Arg Val Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val  
465 470 475

atg aat gta gca atg gtc atg gcc ccg aat ctc ttt atg 1534  
Met Asn Val Ala Met Val Met Ala Pro Asn Leu Phe Met  
480 485

tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa 1573  
Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu  
490 495 500

ttt gta atg gca gct ggg aca gca aat acc atg cac tta 1612  
Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu  
505 510

ttg att aag tac caa aaa ctt ctg tgg aca att ccc aag 1651  
Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys  
515 520 525

ttt att gta aac caa gtg agg aag caa aac acg gaa aat 1690  
Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn  
530 535 540

cat aaa aag gat aaa aga gcc atg aag aaa ttg ctg aag 1729  
His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys  
545 550

aaa atg gct tat gac cga gaa aaa tat gaa aag caa gat 1768  
Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp  
555 560 565

aag agt aca aat gat gct gac gtt cct cag gga gtg att 1807  
Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile  
570 575

cga gtg caa gct ccc cat ctt tcg aaa gtt tcc atg gca 1846  
Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala  
580 585 590

ata cag cta act gaa gaa cta aaa gcc agt gat gta ctt 1885  
 Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu  
           595                          600                          605

gcc agg ttt ctc agc caa gaa agt ggg gtt gcc cag act 1924  
 Ala Arg Phe Leu Ser Gln Glu Ser Gly Val Ala Gln Thr  
                           610                          615

ctc aag aaa gga gaa gtt ttt ttg tat gaa att gga gga 1963  
 Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly Gly  
           620                          625                          630

aat att ggg gaa cgc tgc ctt gat gat gac act tac atg 2002  
 Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met  
                           635                          640

aag gat tta tat cag ctt aac cca aat gct gag tgg gtt 2041  
 Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val  
           645                          650                          655

ata aag tca aag cca ttg t agaagactta acaagctgca 2080  
 Ile Lys Ser Lys Pro Leu  
           660                          663

gataaccatg tggacttctg tcataattct tgctgagtca agagtgtaaa 2130  
 taaaagaaat ggcaggactc atattattca gttgtaccca agtattttta 2180  
 aaatgactct cttaagcctt aaaaagtcac agatttgtgc tgctgccaga 2230  
 attatattaa attattatta atggtattat tagaiaaaaaa aatttctgga 2280  
 gtgagagtaa agaggcttaa ttagtttctg ggcagttttc ttatgctctg 2330  
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<211> 663

<212> PRT

<213> Homo sapiens

<400> 14

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           20                          25                          30

Ala Gly Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr  
           35                          40                          45

Met Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro  
           50                          55                          60

Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met  
           65                          70                          75

Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu  
           80                          85                          90

Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys Glu Pro Asp

95										100					105				
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				110					115					120					
Asn	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Asp	Pro	Gln	Glu	Ser	Ile	Val					
				125					130					135					
Phe	Leu	Ser	Thr	Leu	Thr	Arg	Thr	Gln	Ala	Ala	Ala	Val	Gln	Lys					
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Arg	Val	Glu	Thr	Val	Ser	Gln	Thr	Leu	Arg	Lys	Lys	Asn	Lys	Gln					
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Tyr	Gln	Ile	Pro	Asp	Val	Arg	Asp	Ile	Phe	Ala	Gln	Gln	Arg	Glu					
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Ser	Lys	Glu	Thr	Ala	Pro	Gly	Gly	Thr	Glu	Ser	Gln	Ser	Leu	Arg					
				185					190					195					
Thr	Asn	Glu	Asn	Lys	Tyr	Gln	Gly	Arg	Asp	Asp	Glu	Ala	Ser	Asn					
				200					205					210					
Leu	Val	Gly	Glu	Glu	Lys	Leu	Ile	Pro	Pro	Glu	Glu	Thr	Pro	Ala					
				215					220					225					
Pro	Glu	Thr	Asp	Ile	Asn	Leu	Glu	Val	Ser	Phe	Ala	Glu	Gln	Ala					
				230					235					240					
Leu	Asn	Gln	Lys	Glu	Arg	Ser	Lys	Glu	Lys	Ile	Gln	Lys	Ser	Lys					
				245					250					255					
Gly	Asp	Asp	Ala	Thr	Leu	Pro	Ser	Phe	Arg	Leu	Pro	Lys	Asp	Lys					
				260					265					270					
Thr	Gly	Thr	Thr	Arg	Ile	Gly	Asp	Leu	Ala	Pro	Gln	Asp	Met	Lys					
				275					280					285					
Lys	Val	Cys	His	Leu	Ala	Leu	Ile	Glu	Leu	Thr	Ala	Leu	Tyr	Asp					
				290					295					300					
Val	Leu	Gly	Ile	Glu	Leu	Lys	Gln	Gln	Lys	Ala	Val	Lys	Ile	Lys					
				305					310					315					
Thr	Lys	Asp	Ser	Gly	Leu	Phe	Cys	Val	Pro	Leu	Thr	Ala	Leu	Leu					
				320					325					330					
Glu	Gln	Asp	Gln	Arg	Lys	Val	Pro	Gly	Met	Arg	Ile	Pro	Leu	Ile					
				335					340					345					
Phe	Gln	Lys	Leu	Ile	Ser	Arg	Ile	Glu	Glu	Arg	Gly	Leu	Glu	Thr					
				350					355					360					
Glu	Gly	Leu	Leu	Arg	Ile	Pro	Gly	Ala	Ala	Ile	Arg	Ile	Lys	Asn					
				365					370					375					
Leu	Cys	Gln	Glu	Leu	Glu	Ala	Lys	Phe	Tyr	Glu	Gly	Thr	Phe	Asn					
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Trp	Glu	Ser	Val	Lys	Gln	His	Asp	Ala	Ala	Ser	Leu	Leu	Lys	Leu					
				395					400					405					

Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu	410	415	420
Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln	425	430	435
Leu Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala Asn	440	445	450
Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile	455	460	465
Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met	470	475	480
Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys	485	490	495
Ser Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn	500	505	510
Thr Met His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile	515	520	525
Pro Lys Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn	530	535	540
His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met	545	550	555
Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn	560	565	570
Asp Ala Asp Val Pro Gln Gly Val Ile Arg Val Gln Ala Pro His	575	580	585
Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu Leu Lys	590	595	600
Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly Val	605	610	615
Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly	620	625	630
Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys	635	640	645
Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val Ile Lys Ser	650	655	660

Lys Pro Leu

<210> 15

<211> 1327

<212> DNA

<213> Homo sapiens

<220>

<221> unsure  
 <222> 74, 1306  
 <223> unknown base

<400> 15

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ctttgtgacc agtaccgcaa ggggatcatc tcgggctccg tctgccagga 250

cctgtgtgag ctgcat      atg gtg gag tgg agg acc tgc ctc 290
                        Met Val Glu Trp Arg Thr Cys Leu
                          1          5

tcg gtg gcc ccg ggc cag cag gtg tac agc ggg ctc tgg 329
Ser Val Ala Pro Gly Gln Gln Val Tyr Ser Gly Leu Trp
      10          15          20

cgg gac aag gat gta acc atc aag tgt ggc att gag gag 368
Arg Asp Lys Asp Val Thr Ile Lys Cys Gly Ile Glu Glu
          25          30

acc ctc gac tcc aag gcc cgg tcg gat gcg gcc ccc cgg 407
Thr Leu Asp Ser Lys Ala Arg Ser Asp Ala Ala Pro Arg
      35          40          45

cgg gag ctg gta ctg ttt gac aag ccc acc cgg ggc acc 446
Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr
          50          55          60

tcc atc aag gaa ttc cgg gag atg acc ctc ggc ttc ctc 485
Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu
          65          70

aag gcg aac ctg gga gac ctg cct tcc ctg ccg gcg ctg 524
Lys Ala Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu
      75          80          85

gtt ggc cag gtc ctg ctc atg gct gac ttc aac aag gac 563
Val Gly Gln Val Leu Leu Met Ala Asp Phe Asn Lys Asp
          90          95

aac cgg gtg tcc ctg gcg gaa gcc aag tcc gtg tgg gcc 602
Asn Arg Val Ser Leu Ala Glu Ala Lys Ser Val Trp Ala
      100          105          110

ctg ctg cag cgt aac gag ttc ctg ctg ctg ctg tcc ctg 641
Leu Leu Gln Arg Asn Glu Phe Leu Leu Leu Leu Ser Leu
          115          120          125

cag gag aag gag cac gcc tcc aga ctg ctg ggc tac tgt 680
Gln Glu Lys Glu His Ala Ser Arg Leu Leu Gly Tyr Cys
          130          135

ggg gac ctc tac ctc acc gag ggc gtg ccg cat ggc gcc 719
Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly Ala

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140	145	150	
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Trp His Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu			
155	160		
ctg ccg cct gcc ctg cag ggt gct ctc cag cag tgg ctg			797
Leu Pro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu			
165	170	175	
ggg cct gcg tgg cct tgg cgg gcc aag atc gcc atc ggc			836
Gly Pro Ala Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly			
180	185	190	
ctg ctg gag ttc gtg gag gag ctc ttc cac ggc tct tac			875
Leu Leu Glu Phe Val Glu Glu Leu Phe His Gly Ser Tyr			
195	200		
ggg act ttc tac atg tgt gag acc aca ctg gcc aac gtg			914
Gly Thr Phe Tyr Met Cys Glu Thr Thr Leu Ala Asn Val			
205	210	215	
ggc tac aca gcc acc tac gac ttc aag atg gcc gac ctg			953
Gly Tyr Thr Ala Thr Tyr Asp Phe Lys Met Ala Asp Leu			
220	225		
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Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg Phe Leu			
230	235	240	
cag ggc cgc cgc tgc gag cac agc acc gac tgc acc tac			1031
Gln Gly Arg Arg Cys Glu His Ser Thr Asp Cys Thr Tyr			
245	250	255	
ggg cgc gac tgc agg gcc ccg tgt gac agg ctc atg agg			1070
Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg Leu Met Arg			
260	265		
cag tgc aag ggc gac ctc atc cag ccc aac ctg gcc aag			1109
Gln Cys Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys			
270	275	280	
gtg tgc gca ctg cta cgg ggc tac ctg ctg cct ggc gcg			1148
Val Cys Ala Leu Leu Arg Gly Tyr Leu Leu Pro Gly Ala			
285	290		
ccc gcc gac ctc cgc gag gag ctg ggc aca cag ctg cgc			1187
Pro Ala Asp Leu Arg Glu Glu Leu Gly Thr Gln Leu Arg			
295	300	305	
acc tgt acc acg ctg agc ggg ctg gcc agc cag gtg gag			1226
Thr Cys Thr Thr Leu Ser Gly Leu Ala Ser Gln Val Glu			
310	315	320	
gcc cat cac tcg ctg gtg ctc agc cac ctc aag act ctg			1265
Ala His His Ser Leu Val Leu Ser His Leu Lys Thr Leu			
325	330		
ctc tgg aag aag atc tcc aac acc aag tac tct t g			1300
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<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 104

<223> unknown amino acid

<400> 16

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Gly	Ile	Glu	Glu	Thr	Leu	Asp	Ser	Lys	Ala	Arg	Ser	Asp	Ala	Ala	
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Pro	Arg	Arg	Glu	Leu	Val	Leu	Phe	Asp	Lys	Pro	Thr	Arg	Gly	Thr	
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Ser	Ile	Lys	Glu	Phe	Arg	Glu	Met	Thr	Leu	Gly	Phe	Leu	Lys	Ala	
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Asn	Leu	Gly	Asp	Leu	Pro	Ser	Leu	Pro	Ala	Leu	Val	Gly	Gln	Val	
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Leu	Leu	Met	Ala	Asp	Phe	Asn	Lys	Asp	Asn	Arg	Val	Ser	Xaa	Ala	
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Glu	Ala	Lys	Ser	Val	Trp	Ala	Leu	Leu	Gln	Arg	Asn	Glu	Phe	Leu	
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Leu	Leu	Leu	Ser	Leu	Gln	Glu	Lys	Glu	His	Ala	Ser	Arg	Leu	Leu	
				125					130					135	
Gly	Tyr	Cys	Gly	Asp	Leu	Tyr	Leu	Thr	Glu	Gly	Val	Pro	His	Gly	
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Ala	Trp	His	Ala	Ala	Ala	Leu	Pro	Pro	Leu	Leu	Arg	Pro	Leu	Leu	
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Trp	Pro	Trp	Arg	Ala	Lys	Ile	Ala	Ile	Gly	Leu	Leu	Glu	Phe	Val	
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Met	Ala	Asp	Leu	Gln	Gln	Val	Ala	Pro	Glu	Ala	Thr	Val	Arg	Arg	
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Phe	Leu	Gln	Gly	Arg	Arg	Cys	Glu	His	Ser	Thr	Asp	Cys	Thr	Tyr
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Gly	Arg	Asp	Cys	Arg	Ala	Pro	Cys	Asp	Arg	Leu	Met	Arg	Gln	Cys
				260					265					270
Lys	Gly	Asp	Leu	Ile	Gln	Pro	Asn	Leu	Ala	Lys	Val	Cys	Ala	Leu
				275					280					285
Leu	Arg	Gly	Tyr	Leu	Leu	Pro	Gly	Ala	Pro	Ala	Asp	Leu	Arg	Glu
				290					295					300
Glu	Leu	Gly	Thr	Gln	Leu	Arg	Thr	Cys	Thr	Thr	Leu	Ser	Gly	Leu
				305					310					315
Ala	Ser	Gln	Val	Glu	Ala	His	His	Ser	Leu	Val	Leu	Ser	His	Leu
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Lys	Thr	Leu	Leu	Trp	Lys	Lys	Ile	Ser	Asn	Thr	Lys	Tyr	Ser	
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 1924, 1939, 1953, 1982, 1991-1992, 2000, 2443  
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 attgtaaaaa ttacagagc ggaatcatat gctgggtctcc aagagtttaa 250  
 agcagcctta gaagatttaa atg cag ttc ttt ttc aac ttc 291  
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 Gln Asp Trp Pro Glu Gly Leu Leu Gln Glu Xaa Glu Lys  
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 gta ctc tgc gat gct ggt ttt tta ggt gat gcc tta caa 369  
 Val Leu Cys Asp Ala Gly Phe Leu Gly Asp Ala Leu Gln  
 25 30  
  
 ctc ttt ctt cag tgc tta gcc ctt gat gaa gat ttt gca 408  
 Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe Ala  
 35 40 45  
  
 cct gca aag ctg caa gta caa aag att tta tgt gat tta 447

Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu  
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 Leu Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser  
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tcc tgg agt tca tta cca tgt act aaa aac aga cct ttt 525  
 Ser Trp Ser Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe  
           75                                  80                                  85

gat ttt cat tca gtg atg gaa gag tct cag tct ctc aat 564  
 Asp Phe His Ser Val Met Glu Glu Ser Gln Ser Leu Asn  
                                   90                                  95

gaa cct agc cca aag cag agt gaa gaa ata cca gag gtc 603  
 Glu Pro Ser Pro Lys Gln Ser Glu Glu Ile Pro Glu Val  
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act tca gag cct gtc aaa gga agc tta aac cgt gct cag 642  
 Thr Ser Glu Pro Val Lys Gly Ser Leu Asn Arg Ala Gln  
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tca gca cag tct ata aat tca aca gaa atg cct gcc aga 681  
 Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro Ala Arg  
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gag gac tgt tta aaa aaa gtg tcc tca gaa cct gtt ctg 720  
 Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu  
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tca gtt caa gaa aaa ggt gtt ctg ctg aaa aga aag ttg 759  
 Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu  
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tct ctt tta gaa cag gat gtg att gta aat gaa gat gga 798  
 Ser Leu Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly  
   165                                  170                                  175

aga aat aag ctg aaa aaa caa gga gaa act ccc aat gaa 837  
 Arg Asn Lys Leu Lys Lys Gln Gly Glu Thr Pro Asn Glu  
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gtc tgt atg ttt tcc tta gct tat ggt gat att cca gaa 876  
 Val Cys Met Phe Ser Leu Ala Tyr Gly Asp Ile Pro Glu  
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gaa tta atc gat gtc tca gat ttc gag tgt tct ctc tgc 915  
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 Met Arg Leu Phe Phe Glu Pro Val Thr Thr Pro Cys Gly  
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 His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Asn

245

250

gag tat cta gca gat agg agg tac tgt gtc aca cag ctg 1071  
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 Leu Glu Glu Leu Ile Val Lys Tyr Leu Pro Asp Glu Leu  
 270 275 280

tct gag aga aaa aaa ata tat gaa gaa gaa act gct gaa 1149  
 Ser Glu Arg Lys Lys Ile Tyr Glu Glu Glu Thr Ala Glu  
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ctc tca cac ttg acc aag aat gtt cca ata ttt gtt tgc 1188  
 Leu Ser His Leu Thr Lys Asn Val Pro Ile Phe Val Cys  
 295 300 305

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 Thr Met Ala Tyr Pro Thr Val Pro Cys Pro Leu His Val  
 310 315

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 Phe Glu Pro Arg Tyr Arg Leu Met Ile Arg Arg Ser Ile  
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aca caa aat agt ttt gca gat tat ggt tgt atg tta caa 1344  
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att aga aac gtg cat ttc tta ccg gac gga agg tct gtg 1383  
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 360 365 370

gtt gat aca gtt gga gga aag cgg ttt agg gtt tta aaa 1422  
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 375 380

aga gga atg aaa gat gga tat tgc act gcc gac att gaa 1461  
 Arg Gly Met Lys Asp Gly Tyr Cys Thr Ala Asp Ile Glu  
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 Tyr Leu Glu Asp Val Lys Val Glu Asn Glu Asp Glu Ile  
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 Lys Asn Leu Arg Glu Leu His Asp Leu Val Tyr Ser Gln  
 415 420

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 Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp Arg Phe Arg  
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agc caa att ctt cag cat ttc gga tca atg ccc gag ang 1617  
 Ser Gln Ile Leu Gln His Phe Gly Ser Met Pro Glu Xaa  
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 Glu Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp  
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 Cys Trp Trp Leu Leu Ala Val Leu Pro Val Asp Pro Arg  
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 Tyr Gln Leu Ser Val Leu Ser Met Lys Ser Leu Lys Glu  
 480 485

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 Arg Leu Thr Lys Ile Gln His Ile Leu Thr Tyr Phe Ser  
 490 495 500

aga gac caa tct aag t a actaactctt tggatctccc 1810  
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 Ala Leu Gln Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe  
 35 40 45  
 Ala Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu Leu  
 50 55 60  
 Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser Ser Trp Ser  
 65 70 75  
 Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe Asp Phe His Ser Val  
 80 85 90  
 Met Glu Glu Ser Gln Ser Leu Asn Glu Pro Ser Pro Lys Gln Ser  
 95 100 105  
 Glu Glu Ile Pro Glu Val Thr Ser Glu Pro Val Lys Gly Ser Leu  
 110 115 120  
 Asn Arg Ala Gln Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro  
 125 130 135  
 Ala Arg Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu  
 140 145 150  
 Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu Ser Leu  
 155 160 165  
 Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly Arg Asn Lys Leu  
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 Lys Lys Gln Gly Glu Thr Pro Asn Glu Val Cys Met Phe Ser Leu  
 185 190 195  
 Ala Tyr Gly Asp Ile Pro Glu Glu Leu Ile Asp Val Ser Asp Phe

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Asp	His	Ala	Pro	Tyr	Cys	Pro	Leu	Cys		Lys	Glu	Ser	Leu	Asn	Glu				
				245						250					255				
Tyr	Leu	Ala	Asp	Arg	Arg	Tyr	Cys	Val		Thr	Gln	Leu	Leu	Glu	Glu				
				260						265					270				
Leu	Ile	Val	Lys	Tyr	Leu	Pro	Asp	Glu		Leu	Ser	Glu	Arg	Lys	Lys				
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Ile	Tyr	Glu	Glu	Glu	Thr	Ala	Glu	Leu		Ser	His	Leu	Thr	Lys	Asn				
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Val	Pro	Ile	Phe	Val	Cys	Thr	Met	Ala		Tyr	Pro	Thr	Val	Pro	Cys				
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Pro	Leu	His	Val	Phe	Glu	Pro	Arg	Tyr		Arg	Leu	Met	Ile	Arg	Arg				
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Ser	Ile	Gln	Thr	Gly	Thr	Lys	Gln	Phe		Gly	Met	Cys	Val	Ser	Asp				
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Asn	Val	His	Phe	Leu	Pro	Asp	Gly	Arg		Ser	Val	Val	Asp	Thr	Val				
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Gly	Gly	Lys	Arg	Phe	Arg	Val	Leu	Lys		Arg	Gly	Met	Lys	Asp	Gly				
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Tyr	Cys	Thr	Ala	Asp	Ile	Glu	Tyr	Leu		Glu	Asp	Val	Lys	Val	Glu				
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Asn	Glu	Asp	Glu	Ile	Lys	Asn	Leu	Arg		Glu	Leu	His	Asp	Leu	Val				
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Tyr	Ser	Gln	Ala	Cys	Ser	Trp	Phe	Gln		Asn	Leu	Arg	Asp	Arg	Phe				
				425						430					435				
Arg	Ser	Gln	Ile	Leu	Gln	His	Phe	Gly		Ser	Met	Pro	Xaa	Arg	Glu				
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Glu	Asn	Leu	Gln	Ala	Ala	Pro	Asn	Gly		Pro	Ala	Trp	Cys	Trp	Trp				
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Leu	Leu	Ala	Val	Leu	Pro	Val	Asp	Pro		Arg	Tyr	Gln	Leu	Ser	Val				
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Leu	Ser	Met	Lys	Ser	Leu	Lys	Glu	Arg		Leu	Thr	Lys	Ile	Gln	His				
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tcagtgtgga gtatctcaaa gcctttcagg ctgtccagaa ttttccaacc 200  
aagaagcagc aactacaggg cttttgaacc ctttctttta ctcattcctg 250  
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atataaacca tggtgcagca tggatgatcta actgtgatat gaataaggca 200  
taactaacat ttgcaccgag accagaatta aaaacaaaaa caaactttaa 250  
aagcttagtt ctatattaaa cttcttctct tttcccagat ccttaatggg 300  
tttatactat gcattttttt ttaaaacaaa cacatcatgt caaactataa 350  
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aactggtact gaattgagtt ctccctttac ctttatgtac aattaaatgt 450  
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cctggccaac cagcgccggc agggaaggca ggtctcccag gttcgccttg 150  
aggaaagcca gggatcatct ccggaattcc ttgatggagg tgccccgggt 200  
gggcttggtca aacagtacca gctcccgccg ggggcccgcac ccgaccgggc 250  
cttggaagtcg agggctctct caatgccaca cttgatgggt acatccttgt 300  
cccgccagag cccgctgtac acctgctggc ccggggcaca cgagaagcag 350  
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